



RAW SEQUENCE LISTING

ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/256,156

Art Unit / Team No. : 0186

Date Processed by STIC: 3/16/99

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,

2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/256,156

DATE: 03/16/1999
TIME: 09:22:49

Input Set: I256156.RAW

This Raw Listing contains the General Information
Section and up to first 5 pages.

Does Not Comply
Corrected Diskette Needed

pg 1-5

1 <110> APPLICANT: GILLIES, Stephen D
2 LO, Kin-Ming
3 LAN, Yan
4 WESOLOWSKI, John
5 <120> TITLE OF INVENTION: Enhancing the Circulating Half-life of
6 Antibody-based Fusion Proteins
7 <130> FILE REFERENCE: LEX-003
8 <140> CURRENT APPLICATION NUMBER: US/09/256,156
9 <141> CURRENT FILING DATE: 1999-02-24
10 <150> EARLIER APPLICATION NUMBER: US 60/075,887
11 <151> EARLIER FILING DATE: 1998-02-25
12 <160> NUMBER OF SEQ ID NOS: 8
13 <170> SOFTWARE: PatentIn Ver. 2.0
14 <210> SEQ ID NO 1
15 <211> LENGTH: 447
16 <212> TYPE: PRT
17 <213> ORGANISM: Homo sapiens
18 <220> FEATURE:
19 <223> OTHER INFORMATION: IGG-1 CHAIN C REGION
20 <400> SEQUENCE: 1

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W--> 23 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
24 20 25 30
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26 35 40 45
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28 50 55 60
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30 65 70 75 80
W--> 31 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
32 85 90 95
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34 100 105 110
W--> 35 Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
36 115 120 125
37 Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
38 130 135 140
39 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
40 145 150 155 160
41 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
42 165 170 175
43 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
44 180 185 190

see item 10 on Env
summary
sheet

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45      Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn
46              195                      200                      205
47      Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His
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49      Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val
50      225                      230                      235                      240
51      Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr
52              245                      250                      255
53      Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu
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56              275                      280                      285
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58              290                      295                      300
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60      305                      310                      315                      320
61      Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile
62              325                      330                      335
63      Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro
64              340                      345                      350
65      Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu
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67      Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn
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69      Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser
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71      Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg
72              405                      410                      415
73      Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu
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77 <210> SEQ ID NO 2

78 <211> LENGTH: 443

79 <212> TYPE: PRT

80 <213> ORGANISM: Homo sapiens

81 <220> FEATURE:

82 <223> OTHER INFORMATION: IGG-2 CHAIN C REGION

83 <400> SEQUENCE: 2

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87              20                      25                      30
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89              35                      40                      45
W--> 90      Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
91              50                      55                      60
W--> 92      Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
93              65                      70                      75                      80
W--> 94      Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa

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95
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 97 100 105 110
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 99 115 120 125
 100 Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
 101 130 135 140
 102 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
 103 145 150 155 160
 104 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
 105 165 170 175
 106 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Asn
 107 180 185 190
 108 Phe Gly Thr Gln Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
 109 195 200 205
 110 Thr Lys Val Asp Lys Thr Val Glu Arg Lys Cys Cys Val Glu Cys Pro
 111 210 215 220
 112 Pro Cys Pro Ala Pro Pro Val Ala Gly Pro Ser Val Phe Leu Phe Pro
 113 225 230 235 240
 114 Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr
 115 245 250 255
 116 Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Gln Phe Asn
 117 260 265 270
 118 Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg
 119 275 280 285
 120 Glu Glu Gln Phe Asn Ser Thr Phe Arg Val Val Ser Val Leu Thr Val
 121 290 295 300
 122 Val His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser
 123 305 310 315 320
 124 Asn Lys Gly Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Thr Lys
 125 325 330 335
 126 Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu
 127 340 345 350
 128 Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe
 129 355 360 365
 130 Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu
 131 370 375 380
 132 Asn Asn Tyr Lys Thr Thr Pro Pro Met Leu Asp Ser Asp Gly Ser Phe
 133 385 390 395 400
 134 Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly
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 139 435 440
 140 <210> SEQ ID NO 3
 141 <211> LENGTH: 494
 142 <212> TYPE: PRT
 143 <213> ORGANISM: Homo sapiens
 144 <220> FEATURE:

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/256,156

DATE: 03/16/1999
TIME: 09:22:49

Input Set: I256156.RAW

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146 <400> SEQUENCE: 3

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W--> 149 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
150 20 25 30

W--> 151 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
152 35 40 45

W--> 153 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
154 50 55 60

W--> 155 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
156 65 70 75 80

W--> 157 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
158 85 90 95

W--> 159 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
160 100 105 110

W--> 161 Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
162 115 120 125

163 Ala Pro Cys Ser Arg Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys
164 130 135 140

165 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
166 145 150 155 160

167 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
168 165 170 175

169 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
170 180 185 190

171 Leu Gly Thr Gln Thr Tyr Thr Cys Asn Val Asn His Lys Pro Ser Asn
172 195 200 205

173 Thr Lys Val Asp Lys Arg Val Glu Leu Lys Thr Pro Leu Gly Asp Thr
174 210 215 220

175 Thr His Thr Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro
176 225 230 235 240

177 Pro Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro
178 245 250 255

179 Pro Cys Pro Arg Cys Pro Glu Pro Lys Ser Cys Asp Thr Pro Pro Pro
180 260 265 270

181 Cys Pro Arg Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe
182 275 280 285

183 Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro
184 290 295 300

185 Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val
186 305 310 315 320

187 Gln Phe Lys Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr
188 325 330 335

189 Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Phe Arg Val Val Ser Val
190 340 345 350

191 Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys
192 355 360 365

193 Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser
194 370 375 380

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RAW SEQUENCE LISTING
PATENT APPLICATION US/09/256,156

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Input Set: I256156.RAW

195 Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro
196 385 390 395 400
197 Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val
198 405 410 415
199 Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Ser Gly
200 420 425 430
201 Gln Pro Glu Asn Asn Tyr Asn Thr Thr Pro Pro Met Leu Asp Ser Asp
202 435 440 445
203 Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp
204 450 455 460
205 Gln Gln Gly Asn Ile Phe Ser Cys Ser Val Met His Glu Ala Leu His
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215 <400> SEQUENCE: 4

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219 20 25 30
W--> 220 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
221 35 40 45
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223 50 55 60
W--> 224 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
225 65 70 75 80
W--> 226 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
227 85 90 95
W--> 228 Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
229 100 105 110
W--> 230 Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu
231 115 120 125
232 Ala Pro Cys Ser Arg Ser Thr Ser Glu Ser Thr Ala Ala Leu Gly Cys
233 130 135 140
234 Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser
235 145 150 155 160
236 Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser
237 165 170 175
238 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser
239 180 185 190
240 Leu Gly Thr Lys Thr Tyr Thr Cys Asn Val Asp His Lys Pro Ser Asn
241 195 200 205
242 Thr Lys Val Asp Lys Arg Val Glu Ser Lys Tyr Gly Pro Pro Cys Pro
243 210 215 220
244 Ser Cys Pro Ala Pro Glu Phe Leu Gly Gly Pro Ser Val Phe Leu Phe

Input Set: I256156.RAW

Line	Error/Warning	Original Text
21	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
23	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
25	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
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33	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
35	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly P
84	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
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92	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
94	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
96	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa X
98	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly P
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161	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly P
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230	W "N" or "Xaa" used: Feature required	Xaa Xaa Xaa Xaa Xaa Ala Ser Thr Lys Gly P

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/25/9156

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 2 Wrapped Aminos The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
All text must be visible on page.

- 4 Misaligned Amino Acid The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering between the numbering. It is recommended to delete any tabs and uses spacing between the numbers.

- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) features section that some may be missing.

- 7 Wrong Designation Sequence(s) contain amino acid or nucleic acid designators which are not standard
representations as per the Sequence Rules (Please refer to paragraph 1.822)

- 8 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES) (2) INFORMATION FOR SEQ ID NO:X:
 (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
 This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

- 9 Skipped Sequences Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES) <210> sequence id number
 <400> sequence id number
 000

- 10 Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES) Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 11 Use of <213>Organism Sequence(s) are missing this mandatory field or its response.
(NEW RULES)

- 12 Use of <220>Feature Sequence(s) are missing the <220>Feature and associated headings.
(NEW RULES) Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
 Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
 (Sec. 1.823 of new Sequence Rules)

- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.